

8. (AMENDED) A computer system for quantitating [determining] the viral load, if any, found within samples applied to a microarray and the effect of one or more therapies upon a subject comprising a processor and a memory coupled to said processor, said memory encoding one or more programs, said one or more programs causing said processor to perform the following steps:

[generating a viral diffusion curve based on known viral load studies associated with the therapy of interest;]

identifying hybridization activity from an output pattern from at least two samples applied to at least one microarray;

[calibrating the] generating a viral diffusion curve [based on] using at least two viral load measurements based on the identified hybridization activity;

mapping [each of] the identified hybridization activity to coordinates on the viral diffusion curve [output patterns representative of hybridization activity to respective coordinates]; and

quantitating [determining] the viral load by interpreting the coordinates of the [calibrated] viral diffusion curve.

Please add new claims 26-44.

26. The system of claim 8 wherein the mapping step generates an iterated fractal system to map the hybridization activity onto the viral diffusion curve.

27. The system of claim 8 wherein the generation step employs nonlinear information filtering to generate the viral diffusion curve.

28. The system of claim 27 wherein the nonlinear information filtering employed by the generation step is a nonlinear variant of the Extended Kalman Filter.

29. The system of claim 8 wherein said processor also performs the following steps after the quantitation step, determining whether the therapy of interest has been effective based upon the degree of convergence from one sample to another.

30. A technique for quantitating the viral load, if any, found within samples applied to a microarray, said technique comprising the steps of:

identifying hybridization activity from the output pattern of at least two samples applied to at least one microarray;

generating a viral diffusion curve from at least two viral load measurements based on the identified hybridization activity;

mapping the identified hybridization activity to coordinates on the viral diffusion curve; and

quantitating the viral load by interpreting the coordinates of the viral diffusion curve.

31. The technique of claim 30 wherein the viral diffusion curve is generated by populating a Fokker-Planck equation with the viral load measurements.

32. The technique of claim 31 wherein the Fokker-Planck equation utilized to generate the viral diffusion curve is dependent upon the utilized microarray.

33. The technique of claim 30 wherein the mapping step utilizes fractal filtering to map the identified hybridization activity to coordinates on the viral diffusion curve.

34. The technique of claim 30 wherein the generation step employs nonlinear information filtering.

35. The technique of claim 34 wherein the employed nonlinear information filtering is a nonlinear variant of the Extended Kalman Filter.

36. A computer system for quantitating the viral load, if any, found within a sample applied to a microarray comprising a processor and a memory coupled to said processor, said memory encoding one or more programs, said one or more programs causing said processor to perform the following step:

determining the viral load based upon the microarray output patterns generated from the sample applied to the microarray.

37. The system of claim 36 wherein said programs determine viral load by the following technique:

identifying hybridization activity from the output pattern of at least two samples applied to at least one microarray;

generating a viral diffusion curve from at least two viral load measurements based on the identified hybridization activity;

mapping the identified hybridization activity to coordinates on the viral diffusion curve; and

quantitating the viral load by interpreting the coordinates of the viral diffusion curve.

38. The system of claim 36 wherein said programs determine viral load by the following technique:

generating a viral diffusion curve associated with a therapy of interest;

mapping each of the output patterns on the viral diffusion curve;

determining a degree of convergence between the mapped coordinates on the viral diffusion curve; and

determining whether the therapy of interest has been effective based upon the degree of convergence from one sample to another.

39. The system of claim 36 wherein the viral load determination is based on an indicator selected from the group consisting of RNA, DNA, or p24 antigen in plasma.

40. The system of claim 36 wherein said programs determine viral load for use in determining the effectiveness of a therapy.

41. A system for quantitating viral load, if any, within a biological sample comprising:

- a microarray having the biological sample applied thereto;
- a microarray scanner for scanning the output pattern of the microarray; and
- a computation unit for determining the viral load within the sample by analyzing the microarray output pattern.

42. The system of claim 41 wherein said computation unit includes:

- a viral diffusion curve generator for generating a viral diffusion curve associated with a therapy of interest;

- a mapping unit for mapping each of the output patterns representative of hybridization activity to respective coordinates on the viral diffusion curve; and

- a convergence determination unit for determining a degree of convergence between the mapped coordinates on the viral diffusion curve for determining whether the therapy of interest has been effective based upon the degree of convergence from one sample to another.

43. The system of claim 42 wherein said computation unit includes:

- diffusion curve generation means for generating a viral diffusion curve associated with a therapy of interest;

- mapping means for mapping each of the output patterns to respective coordinates on the viral diffusion curve; and

- quantitation means for quantitating the level of viral load within the sample.

44. The system of claim 42 wherein said computation unit includes:

- an interferometer for interferometrically enhancing the output pattern to determine the viral load within the sample.